

GENETICS

Resequencing 'Eve'

Sarsani, V.K. et al. *G3 (Bethesda)* **9**, 1795–1805 (2019)

The genome of the laboratory mouse was first sequenced in 2002; since then, that reference genome—based on C57BL/6J mice and referred to as GRCm38—has been the basis of many projects that rely on mouse genetics. It's been updated over the years, but gaps remain. Sequencing technology has also changed, and today's C57BL/6J mice are now 26 generations (or more) removed from the animals originally sampled to create that first reference.

Time for an update? Researchers at the Jackson Laboratory recently completed a de novo assembly, created with modern long and short read sequencing technologies as well optical mappings, of a mouse called Eve, the 'mother' of current C57BL/6J mice. With their resequenced genome, they note several areas of genetic variation that differ from the current reference and also annotate some new details about the frequently studied strain. *EPN*

<https://doi.org/10.1038/s41684-019-0362-2>

PAIN

Noxious or not? Depends on the rodent

Eigenbrod, O. et al. *Science* **364**, 852–859 (2019)

Pain: some rodents feel it; others...don't, according to new research in *Science* that explores nociception in eight subterranean African rodents.

From prior work, naked mole rats are known to react negatively to an ingredient in mustard oil known as AITC but show notable insensitivity to capsaicin and hydrogen chloric acid, compounds that will elicit pain responses in both humans and traditional lab rodents. Wondering if there's an evolutionary element that might explain why some compounds prove noxious but others benign, a team of researchers tested pain responses in eight of the naked mole rat's close relatives. Sensitivities to the trio of triggers varied among the different species, as did expression of a number of genes. Ion channels appear to play a particular role in mediating pain sensitivity. *EPN*

<https://doi.org/10.1038/s41684-019-0363-1>

ORGANOGENESIS

Organ origins across animals

Cardoso-Moreira, M. et al. *Nature* <https://doi.org/10.1038/s41586-019-1338-5> (2019)

Researchers interested in exploring the evolutionary origins of different organs have a large new transcriptomic resource available. The RNA sequencing effort from the Kaessmann lab at Heidelberg University was published recently in *Nature* and consists of gene expression data for seven organs (cerebrum; cerebellum; heart; kidney; liver; ovary; and testes) sampled from seven species (human; rhesus macaque; mouse; rat; rabbit; opossum; and red junglefowl chicken) across several time points, from prenatal development through adulthood.

The researchers' initial analysis of all that transcriptomic data suggests that the genes involved in organogenesis are similar between species early on in development. However, expression patterns start to change and diverge with age as the animals develop their unique organ features.

All of the data can be accessed online at <http://evodevoapp.kaessmannlab.org>. *EPN*

<https://doi.org/10.1038/s41684-019-0364-0>

ANIMAL BEHAVIOR

About time

Bodden, C. et al. *Sci. Rep.* **9**, 8247 (2019)

To combat issues with reproducibility in animal research, some researchers suggest that rather than trying to standardize as many variables as possible, it might be better to actually switch things up—a concept known as systematic heterogenization. But what variables should—and feasibly can—be varied? A new report in *Scientific Reports* takes a look at timing.

The researchers conducted several behavioral tests of anxiety and exploratory behavior in female mice from two different strains—C57BL/6J and DBA/2N—at three different testing times: in the morning, at noon, and in the afternoon. The researchers observed behavioral variability between the strains depending on the time—most notably between morning and afternoon tests—but show that simply testing animals across time points can improve the reproducibility of results between replicate experiments. *EPN*

<https://doi.org/10.1038/s41684-019-0365-z>

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